Adaptation to synchronization in phase-oscillator networks

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Abstract

We introduce an adaptation algorithm by which an ensemble of coupled oscillators with attractive and repulsive interactions is induced to adopt a prescribed synchronized state. While the performance of adaptation is controlled by measuring a macroscopic quantity, which characterizes the achieved degree of synchronization, adaptive changes are introduced at the microscopic level of the interaction network, by modifying the configuration of repulsive interactions. This scheme emulates the distinct levels of selection and mutation in biological evolution and learning.

Key words: Collective behaviour, natural evolution, learning
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1 Introduction

The emergence of coherent collective behaviour, out of the interaction of a large number of active elements with relatively simple individual dynamics, is the key signature of a complex system [1]. The nature of the mechanisms which underly such emergence, however, can substantially vary between different systems. In physical or chemical phenomena –for instance, in the formation of spatiotemporal patterns in reacting fluids– collective behaviour is the unavoidable, spontaneous consequence of elementary mechanical processes occurring at microscopic scales. In biological systems, on the other hand, collective behaviour is not just the macroscopic manifestation of the mutual organization of

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microscopic entities. It is, as well, the consequence of a much longer evolutionary process, by which certain macroscopic traits are selected at the expense of others, while they change from one generation to the next according the laws of heredity. The joint action of natural selection and mutations, as described by the Darwinian theory of evolution, makes it possible that, in a given environment, the collective performance of a class of biological complex systems –a species– improves as generations succeed each other. Similarly, the acquisition of certain forms of behaviour by learning implies a process by which the response of a living being to given stimuli becomes specific and optimized.

It is interesting that –both in evolution and in learning– the mechanism of selection, on one hand, and the changes that eventually improve performance, on the other, act at very distinct levels. Natural selection of beneficial traits, as well as evaluation of learnt tasks, take place at macroscopic scales, at the level of the organic interaction of individuals with their environment. Variation processes, in contrast, take place at microscopic scales, genetic for evolution and neural for learning. It is precisely the emergent nature of macroscopic traits which connects the two levels.

In this paper, we explore the possibility of emulating this scenario with a rather simple model, based on the collective dynamics of coupled oscillators. It is well known that ensembles of interacting oscillators may undergo self-organization processes which lead to different forms of synchronized behaviour [2,3]. A variety of collective states –in the form of single or multiple synchronized clusters, for instance– can be realized by altering the pattern of interactions between oscillators. We exploit this behavioral diversity for inducing an oscillator ensemble to adopt a specific, target synchronization state, through adaptive introduction of gradual changes in its interaction pattern. Imitating biological adaptation, achievement of the goal is evaluated through a macroscopic measure of synchronization, while changes are introduced at the microscopic level of pair interactions.

We analyze, in the next section, the possible synchronization states of an oscillator ensemble with both attractive and repulsive interactions. We show that if repulsive interactions are conveniently distributed, the ensemble splits into two synchronized clusters with opposite phases. Choosing this two-cluster configuration as the target state, in Section 3 we apply an adaptation algorithm to induce an ensemble, whose repulsive interactions are initially distributed at random, to modify its interaction pattern in such a way that its collective behaviour approaches the target. This formulation contrasts with previous studies of network adaptation to self-organization [4], where the degree of synchronization is evaluated at local –not collective– level. In spite of the huge number of possible ways of distributing the repulsive interactions, our system manages to satisfactorily achieve its goal.

2 Oscillator networks with repulsive interactions

We consider a Kuramoto-like model for N coupled phase oscillators, governed by the equations [2,5]

$$\dot{\phi}_i = \omega_i + \frac{K}{N}\sum_{j=1}^{N} W_{ij}\sin(\phi_j - \phi_i), \tag{1}$$

where $\phi_i(t) \in [0, 2\pi)$ is the phase of oscillator i, and ω_i is its natural frequency. The positive constant K measures the coupling between oscillators, and $W_{ij} = \pm 1$ defines the sign of the interaction between oscillator i and j. Positive and negative W_{ij} represent, respectively, attractive and repulsive "forces" between oscillators. Interactions are assumed to be symmetric, so that $W_{ij} = W_{ji}$. In the following, it will be useful to conceive the interaction pattern as defining a network with vertices occupied by the oscillators, whose links join oscillators with attractive interactions. The complementary network, with links corresponding to repulsive interactions, provides an alternative representation [6].

It is well-known that in the case of global attractive coupling, $W_{ij} = 1$ for all i and j, and in the thermodynamical limit, $N \to \infty$, the oscillator ensemble undergoes a synchronization transition as the coupling strength K grows [2]. This transition is quantified by the Kuramoto order parameter

$$z = \frac{1}{N}\left\langle \left| \sum_{j=1}^{N} \exp(\mathrm{i}\phi_j) \right| \right\rangle, \tag{2}$$

where $\langle\cdot\rangle$ indicates averages over sufficiently long times. Below the critical coupling strength K_c, phases are uniformly distributed in $[0, 2\pi)$, so that $z = 0$. Above K_c, on the other hand, z grows monotonically with K, revealing a progressive condensation of phases. At the same time, an increasingly large cluster of synchronized oscillators, whose time-averaged frequencies,

$$\Omega_i = \left\langle \dot{\phi}_i \right\rangle = \lim_{T\to\infty} \frac{1}{T}\int_0^T \dot{\phi}_i(t)dt, \tag{3}$$

are mutually identical, dominates the collective dynamics of the ensemble. The critical point K_c depends on the distribution of natural frequencies ω_i: a higher dispersion in the natural frequencies requires a stronger coupling to synchronize the ensemble. For asymptotically large K, the cluster of synchronized oscillators entrains the whole ensemble, and all the phases collapse to the same value, so that $z \to 1$.

As it may be expected, when some of the interactions are repulsive, synchronization is harder to attain. This was originally confirmed by Daido [7], who studied Eqs. (1) in the case where the symmetric weights W_{ij} are drawn at random from a Gaussian distribution centered at zero. Moreover, it turns out that the emerging patterns of collective behavior depend crucially on the form in which repulsive interactions are distributed over the ensemble. In Ref. [6], the effect of a random (Erdős-Rényi [8]) network of repulsive interactions was studied for identical phase oscillators ($\omega_i \equiv \omega$ for all i). It was shown that, as the number of repulsive interactions grows, fully synchronized ensembles undergo a sharp transition to desynchronization. Figure 1, on the other hand, shows results for ensembles of $N = 10^3$ *nonidentical* oscillators with an Erdős-Rényi network of repulsive interactions. Natural frequencies are drawn at random from a Gaussian distribution $g(\omega) = \exp(-\omega^2/2)/\sqrt{2\pi}$. Each interaction weight is given by

$$W_{ij} = W_{ji} = \begin{cases} 1 \text{ with probability } 1 - x, \\ -1 \text{ with probability } x, \end{cases} \tag{4}$$

so that x is the average fraction of repulsive interactions. The plot displays the order parameter z, Eq. (2), as a function of the coupling strength K for several values of the fraction x. Note that $x < 1/2$ in all cases, so that the number of attractive interactions is always larger than that of repulsive interactions.

From Kuramoto's theory [2], it is known that in the absence of repulsive interactions ($x = 0$) the synchronization transition for the present distribution of natural frequencies takes place at $K_c \approx 1.6$. Our results show that, as x grows, the transition shifts to higher values of K, and the transition zone becomes broader. Nevertheless, for sufficiently large coupling intensities, the order parameter seems to approach its maximum value, $z = 1$, which corresponds to the state of full synchronization. Thus, as coupling becomes stronger, the more abundant attractive interactions overcome the effect of repulsive interactions, and the whole ensemble aggregates into a single cluster with well-defined phase.

Other modes of collective behaviour can be expected if, instead of being random, the networks of attractive and repulsive interactions are given some special structure. Specifically, consider that the oscillator ensemble is divided into two groups, such that inside each group all interactions are attractive, whereas they are repulsive between oscillators of different groups. In this situation, the network of attractive interactions is fully connected inside each group, and the

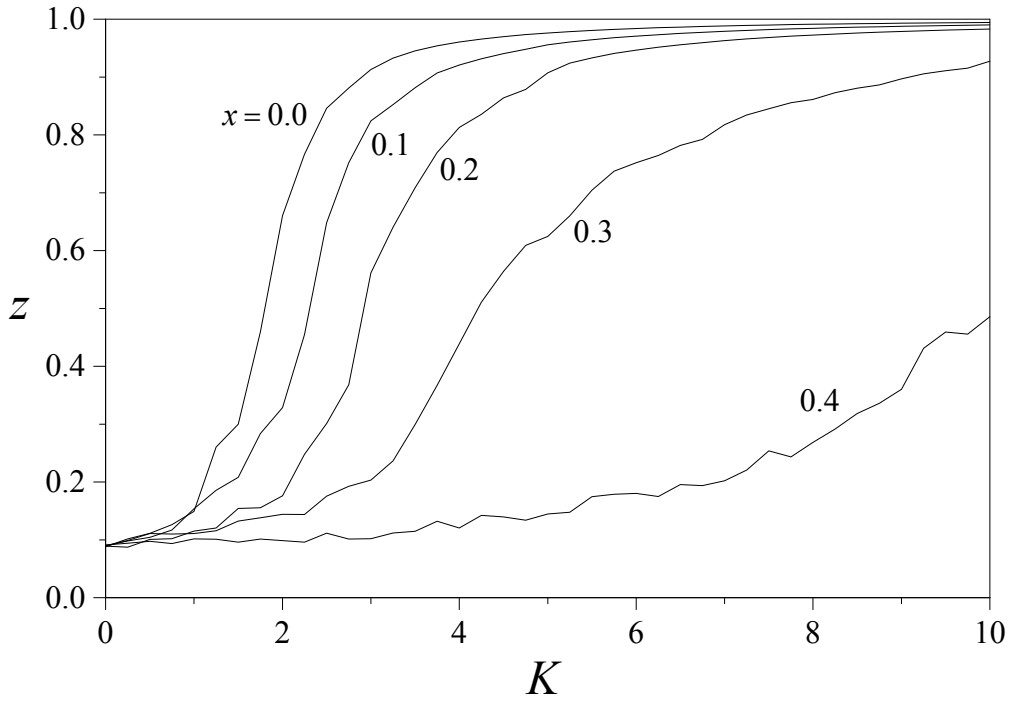

Fig. 1. The Kuramoto order parameter z as a function of the coupling strength K, for an ensemble of 10^3 oscillators with a fraction x of repulsive interactions distributed at random. Repulsive interactions define an Erdős-Rényi network over the oscillator ensemble.

two groups are mutually disconnected. The interaction weights are given by

$$W_{ij} = \begin{cases} 1, \text{ if } i \text{ and } j \text{ belong to the same group,} \\ -1, \text{ otherwise.} \end{cases} \tag{5}$$

If the groups have, respectively, N_1 and N_2 oscillators ($N_1 + N_2 = N$), the fraction of repulsive interactions is $x = 2N_1N_2/N(N-1)$, or equivalently,

$$N_{1,2} = \frac{N}{2}\left[1 \pm \sqrt{1 - 2x(N-1)/N}\right] \approx \frac{N}{2}\left(1 \pm \sqrt{1-2x}\right), \tag{6}$$

where the approximation holds for large N. Note that these numbers make sense if $x < N/2(N-1) \approx 1/2$.

It can be easily realized that, if all natural frequencies are equal ($\omega_i \equiv \omega$ for all i), the only stable solution to Eqs. (1) with the interactions given by Eq. (5) corresponds to all the oscillators of each group having exactly the same phase, and the two groups having opposite phases. In other words, an ensemble of identical oscillators with the interactions of Eq. (5) splits into two point-like opposite clusters in the phase coordinate, each cluster corresponding to one

group. When natural frequencies are not mutually identical, we expect that the clusters spread in phase but, for large coupling strengths, the division into two opposite phase clusters corresponding to the groups should persist. This is in fact what numerical results show. Figure 2 displays results for the order parameter z as a function of the coupling strength K for several values of x, with the distribution of interactions given by Eq. (5), in a system of $N = 10^3$ oscillators. Note that, now, the transition to synchronized behaviour occurs always at the same value of K. On the other hand, the asymptotic value of z for large K depends on x. Indeed, as discussed above, for large K the ensemble is organized in two point-like clusters of opposite phase so that, according to Eq. (2), the order parameter equals

$$z(K \to \infty) = \frac{|N_1 - N_2|}{N} = \sqrt{1 - 2x(N-1)/N} \approx \sqrt{1-2x}, \tag{7}$$

an analytical prediction which is in full agreement with numerical results.

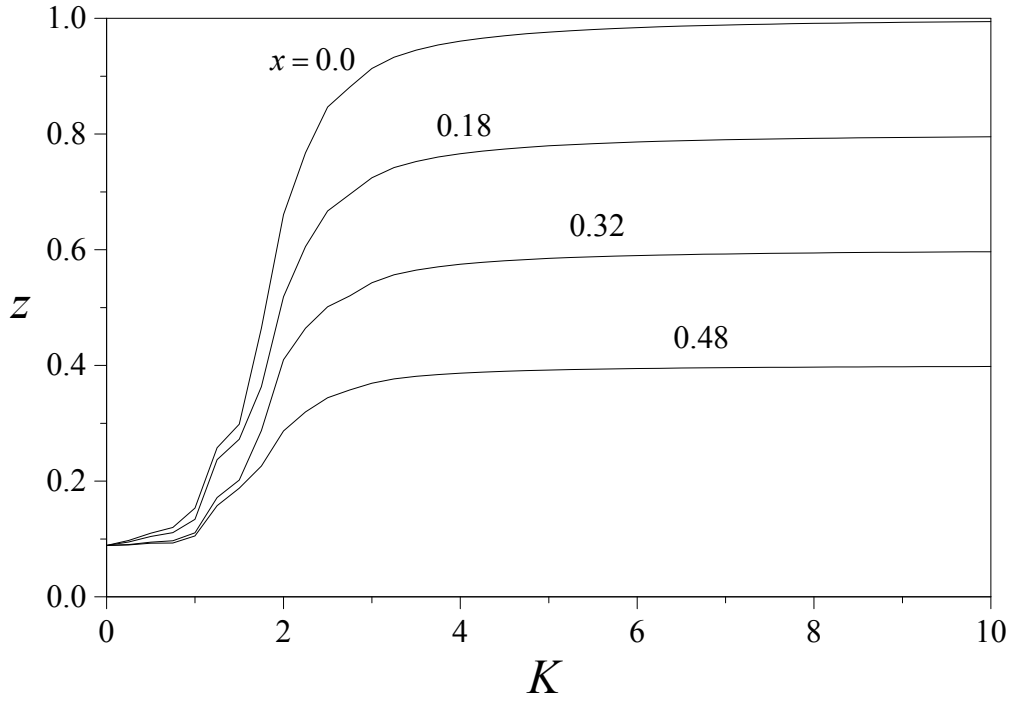

Fig. 2. The Kuramoto order parameter z as a function of the coupling strength K, for an ensemble of 10^3 oscillators divided into two groups. The interaction between two oscillators is attractive (repulsive) if they (do not) belong to the same group. The sizes N_1 and N_2 of the two groups are given, as a function of the fraction x of repulsive interactions, by Eq. (6).

The splitting of the ensemble into two clusters is quantitatively revealed by an additional order parameter [9],

$$z_2 = \frac{1}{N}\left\langle \left| \sum_{j=1}^{N} \exp(2\mathrm{i}\phi_j) \right| \right\rangle \tag{8}$$

[cf. Eq. (2)], which vanishes if oscillator phases are uniformly distributed in $[0, 2\pi)$, and attains its maximum, $z_2 = 1$, if oscillators form two point-like clusters of opposite phases. In this limit, z_2 is independent of the relative size of the two clusters, so that $z_2 = 1$ also in the extreme case of a single point cluster –equivalent to $N_1 = N$ and $N_2 = 0$, or *vice versa*. Therefore, for a random interaction network, both z and z_2 approach unity as the coupling strength grows. It can be easily shown that, in this case, $z > z_2$. For the two-group network, on the other hand, z_2 tends to unity, while z approaches the asymptotic value quoted in Eq. (7) so that, for large K, $z < z_2$. This is illustrated in Fig. 3, for a fixed value of the fraction x of repulsive interactions. The combined analysis of z and z_2 as a function of K thus discerns between the two different forms of collective behaviour of the oscillator ensemble, derived from the different structures of their interaction networks.

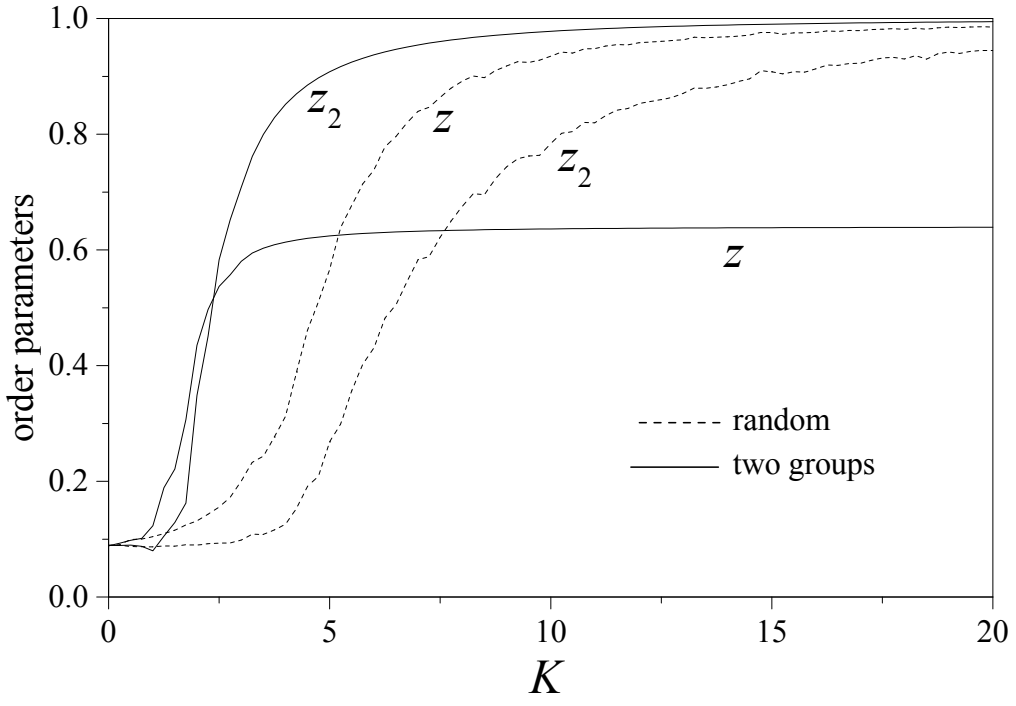

Fig. 3. The order parameters z and z_2 as functions of the coupling strength K, for an ensemble of 50 oscillators with a fraction $x = 0.3$ of repulsive interactions distributed at random (dashed lines) or between two groups (full lines).

3 Adaptation to collective organization

In the preceding section, we have shown that a specifically structured interaction network induces splitting of the oscillator ensemble into two synchronized clusters with opposite phases. In contrast, a random distribution of attractive and repulsive interactions gives rise to a single synchronized cluster. Suppose now to have an ensemble with randomly distributed interactions. Would it be possible, following our discussion in the Introduction, to adaptively evolve the interaction pattern toward the two-group structure by applying selection pressure at the level of collective behaviour? This would amount to modifying microscopic attributes by selection of macroscopic features, as in biological evolution and learning.

In order to explore this possibility, we implement an algorithm of adaptation of the interaction pattern based on a Monte Carlo scheme. The algorithm is controlled by monitoring the collective dynamical state of the oscillator ensemble, as quantified by the two-cluster order parameter z_2. We work at intermediate values of the coupling strength, where the difference in z_2 between the two dynamical modes studied above is larger (cf. Fig. 3). In this intermediate region, coupling is sufficiently strong to induce synchronized collective behaviour, but does not reach the regime where oscillators are confined to almost point-like clusters. In our calculations, we choose $K = 4$.

We start from an interaction pattern with a fraction x of repulsive interactions distributed at random all over the ensemble, with weights W_{ij}. Equations (1) are solved by means of an Euler algorithm, with time increment $h = 0.1$. The system is left to evolve for a few hundred time units (typically, $T = 250$) so that z_2 attains a well-defined value. Then, a small change is introduced in the interaction pattern. Two oscillator pairs, $\{k, l\}$ and $\{r, s\}$, with interactions of opposite signs, $W_{kl} = 1$ and $W_{rs} = -1$, are chosen at random and their interaction weights are interchanged, so that $W'_{kl} = -1$ and $W'_{rs} = 1$. This procedure is repeated on n_P randomly chosen oscillator pairs. With this new interaction pattern, the system evolves again and a new value of the two-cluster order parameter, z'_2, is determined. If $\Delta z_2 = z'_2 - z_2 > 0$, the change in the interaction weights is accepted. If on the other hand, $\Delta z_2 < 0$, the change is accepted with probability $\exp(\Delta z_2/\theta)$, and rejected otherwise. The fictitious temperature θ is used to control the speed of the adaptation process. The algorithm is repeated a number of times (typically, several hundred), until the successive values of z_2 converge to a stationary level. Following the standard Monte Carlo practice, the temperature θ is slowly decreased as the process progresses, to gradually attenuate the effect of fluctuations in z_2. In our simulations, the number of pairs whose interaction weights are modified at each adaptation step is around $n_P = 10$, and is adjusted to make the final value of z_2 as large as possible.

To illustrate our results, we consider a realization of the above Monte Carlo process in an ensemble of $N = 50$ oscillators, where the fraction of repulsive interactions is $x = 3/7 \approx 0.43$. In a two-group interaction network, this would correspond to groups of sizes $N_1 = 15$ and $N_2 = 35$. From an initial value $z_2 \approx 0.14$, obtained for a random interaction network, the two-cluster order parameter significantly increases by a factor slightly above four, reaching $z_2 \approx 0.57$. Numerical results for systems of this size, with $K = 4$ and the two-group structure given by the interaction weights of Eq. (5), show however that the two-cluster order parameter can reach values around $z_2 = 0.9$. After the Monte Carlo process, the obtained value of z_2 is still considerably below this level. In any case, in order to evaluate to which extent has the system evolved towards the target state, we examine both its resulting dynamical behaviour and its interaction pattern.

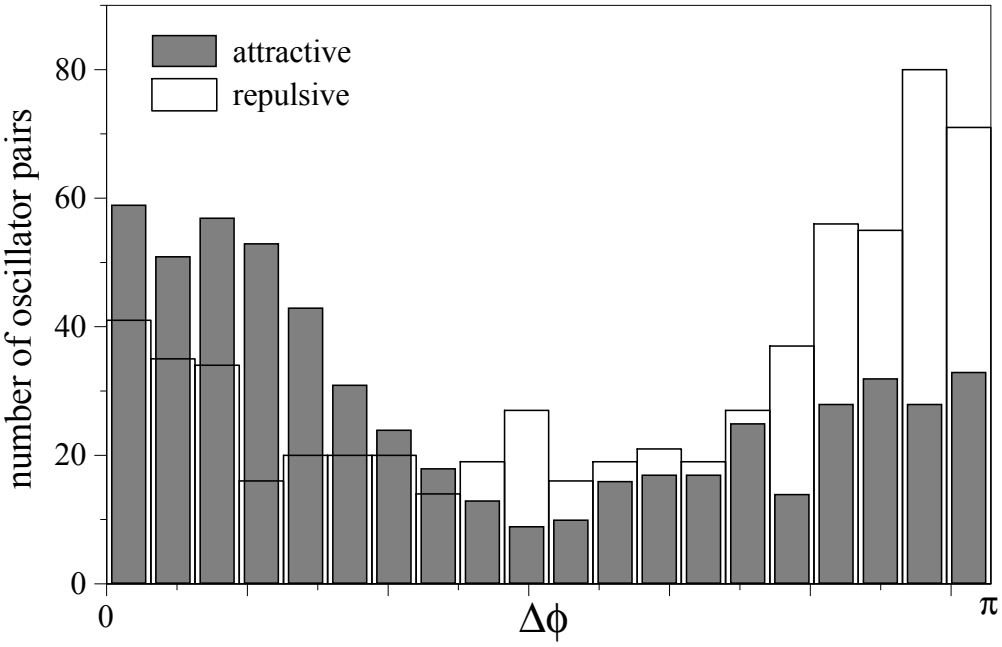

Fig. 4. Number of oscillator pairs $\{i, j\}$ with relative phase $\Delta\phi_{ij} = |\phi_i - \phi_j|$, and attractive or repulsive interactions. Individual phases were measured at a fixed time after adaptation to the two-group state, in a realization with the parameters quoted in the text.

3.1 Distribution of phases and synchronization

Figure 4 shows results illustrating the correlation between the relative phase of each oscillator pair and the sign of the corresponding interaction, after adaptation. For two oscillators i and j, the relative phase $\Delta\phi_{ij} = |\phi_i - \phi_j|$ should be close to 0 or π for $W_{ij} = 1$ or -1, respectively. Indeed, as expected, the his-

tograms of Fig. 4 display a clear excess of attractive (repulsive) interactions for small (large) relative phases. A quantitative measure of the correlation between $\Delta\phi_{ij}$ and W_{ij} is given by the index

$$C = \frac{2}{N(N-1)} \sum_{i,j>i} W_{ij} \cos \Delta\phi_{ij}. \tag{9}$$

It is easily shown that, for the synchronized state with two point clusters – which would be achieved for large coupling strengths and a perfect two-group interaction network– we get $C = 1$. When oscillators are uniformly spread in phases, on the other hand, $C \sim N^{-1}$. The latter is the expected value of C for a random interaction network. In fact, from Fig. 1, we note that for the present values of x and K the oscillator ensemble with randomly distributed repulsive interactions is essentially unsynchronized. For the data corresponding to Fig. 4, in contrast, we find $C \approx 0.22$. As may have been expected, due to the moderate coupling strength, this is still far from the maximum. However, C is an order of magnitude larger than the value expected for an unsynchronized ensemble. This indicates that adaptation has had a substantial effect in the desired direction.

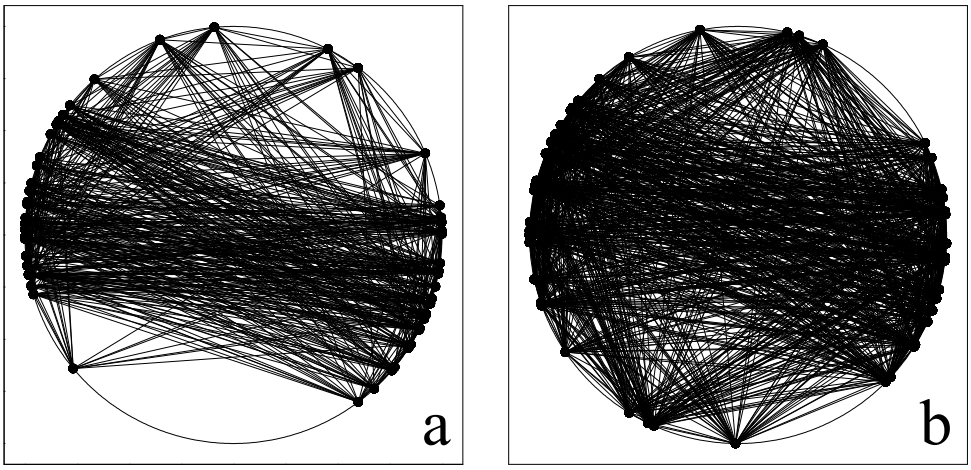

Fig. 5. Two snapshots of the distribution of phases after adaptation to the two-group state, in an ensemble of 50 oscillators with the parameters specified in the main text. Individual phases are represented over the unit circle, and lines stand for repulsive interactions between oscillators.

Closer inspection of the distribution of phases reveals a complementary consequence of the moderate value of K. The two plots of Fig. 5 are representations of the individual phases of the 50 oscillators over the unit circle. Lines joining oscillators represent repulsive interactions. Each plot corresponds to a different time, i.e. it shows a snapshot of the distribution of phases. In Fig. 5a, it is clear that most of the ensemble has split into two clusters with approximately opposite phases, with most of the repulsive interactions standing between os-

cillators in different clusters. Some time later, as illustrated by the snapshot of Fig. 5b, clusters are however much less defined and the distribution over the unit circle is more uniform. While most of the repulsive interactions still correspond to pairs of oscillators with opposite phases, it is clear that the ensemble is considerably more spread.

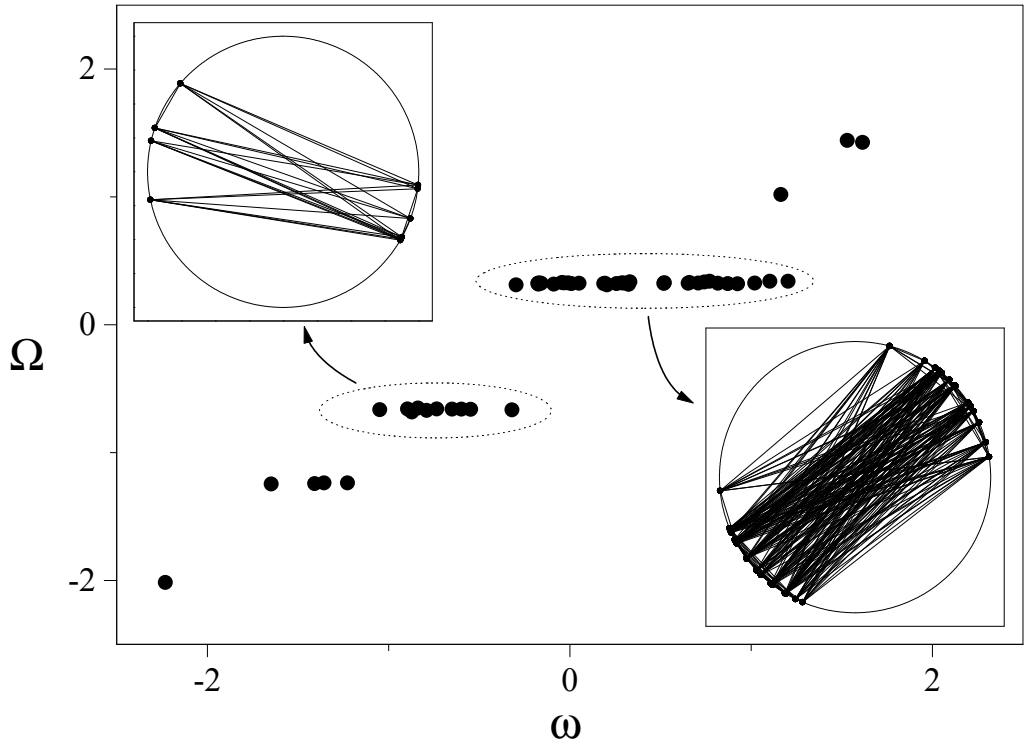

Fig. 6. Main plot: The average frequency Ω_i as a function the natural frequency ω_i for individual oscillators after adaptation, with the parameters specified in the main text. Inserts: Snapshots of the distribution of phases (cf. Fig. 5) for the synchronized clusters inside dotted frames.

To disclose the origin of this apparent time variation in the degree of organization in phases, it is useful to consider as well the distribution of frequencies over the ensemble. The main plot in Fig. 6 represents the average frequency Ω_i, defined in Eq. (3), as a function of the natural frequency ω_i for each individual oscillator. In this kind of plot, horizontal arrays of dots represent clusters of oscillators whose natural frequencies are different, but which have synchronized to a common average frequency. At the present value of K, we find several of these clusters, of different sizes, with different average frequencies. The analysis of the distribution of repulsive interactions inside each synchronized cluster shows that the adaptation algorithm has in fact succeeded at separating groups with opposite phases. This is displayed for two of the synchronized clusters in the inserts of Fig. 6. However, since each synchronized cluster has its own average frequency, they move around the unit circle with respect to each other. Thus, their relative position changes, and the clustering

in the distribution of phases is at times more evident, at times less defined. This observation brings to light a subtle difference between the goal of the adaptation algorithm and the synchronization of the ensemble: for intermediate values of the coupling strength, pairs of clusters with opposite phases form due to the redistribution of repulsive interactions, though desynchronization between different pairs may persist.

3.2 Structure of the interaction network

The results discussed in Section 3.1 allow us to appraise the performance of adaptation at the level of the dynamical state achieved by the ensemble, through the correlation between phases and the distribution of repulsive interactions, and through the degree of synchronization. This macroscopic viewpoint can be complemented by an evaluation of the microscopic structure of the resulting interaction network. In other words, we aim at evaluating to which extent the redistribution of interactions has transformed the initial random structure into the two-group target. However, if such evaluation is purely based on an analysis of the network structure, the resulting distribution of phases must be disregarded. This has the drawback that we do not know *a priori* which oscillators belong to each group.

To tackle this problem we have adapted two algorithms of community detection in networks [10,11], whose aim is to identify groups of network nodes which are internally best connected. In our case, this task is translated into the identification of two groups which maximize the number of attractive interactions inside each group. The result is given as an ordering of the oscillators, with lower ranks corresponding to one group and higher ranks to the other. In the first method, called spectral partitioning algorithm [10], the size of the two groups is fixed –in our case, to $N_1 = 15$ and $N_2 = 35$. In the second, which is based on the maximization of the network modularity [11], the group size is free.

Figure 7a is a graphical representation of the adjacency matrix of the network of attractive interactions with the numbering resulting from the first method. Squares represent oscillator pairs with attractive interactions. In the ideal case where both the adaptation algorithm and the ordering method are perfectly successful, all squares should be concentrated in two non-overlapping blocks of sizes $N_1 \times N_1$ and $N_2 \times N_2$, situated along the diagonal. Though our result is far from this ideal configuration, a larger density of squares is apparent over the two blocks. Figure 7b presents the result of using the second method, with free group sizes. The concentration in the expected zones is again clear, though the resulting groups are of slightly different sizes: $N_1 \approx 20$ and $N_2 \approx 30$.

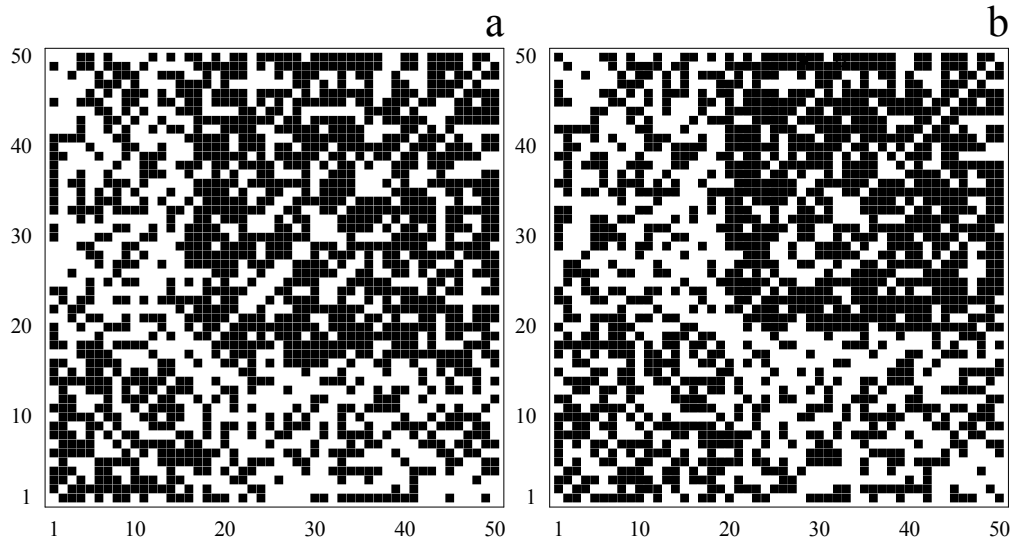

Fig. 7. Graphical representation of the adjacency matrices of the network of attractive interactions, after detection of the two groups, (a) by the algorithm of spectral partitioning and (b) by maximizing the network modularity.

In order to quantify the performance of adaptation at the level of the network structure, we may use the results depicted in Fig. 7 to introduce an index which measures to what extent has the adjacency matrix achieved the ideal division into two blocks. Let f be the fraction of sites inside the blocks (excluding the diagonals) which are occupied by squares after adaptation, and $f_R = 1 - x$ the fraction of occupied sites for a random distribution of attractive interactions. Note that f_R coincides, up to random fluctuations, with the fraction of occupied sites inside the blocks in the initial condition. We define

$$D = \frac{f - f_R}{1 - f_R}. \tag{10}$$

In the ideal final state, we would have $D = 1$, because the filling of the two blocks would be perfect ($f = 1$). Meanwhile, for randomly distributed interactions, $f \approx f_R$ and $D \approx 0$. Taking into account the effect of fluctuations, in fact, we find $D \sim N^{-1}$. The values of D calculated for the results shown in Fig. 7 are (a) $D = 0.26$ and (b) 0.33. As for the case of the index C, Eq. (9), these values are considerably smaller than the ideal. However, during adaptation, they have grown by an order of magnitude, which represents an important improvement towards the target interaction pattern.

4 Discussion and conclusion

For the 50-oscillator ensemble, we have repeated the analysis with groups of various sizes ($N_1 = 10$, 20, 25) and a different coupling strength ($K = 8$), and have always obtained consistent results –not presented here for conciseness. The degree of adaptation both in dynamics and in network structure, as measured by the quantities C and D, was similar to that presented above. We have also tested the adaptation algorithm using the difference $\zeta = z_2^2 - z^2$, instead of the two-cluster order parameter z_2, as the macroscopic measure of collective organization. In view of the results displayed in Fig. 3, this criterion is expected to exhibit better performance for large values of K, where the difference between the two order parameters z and z_2 is large for the two-group configuration, and small for the random interaction network. Finally, we have verified that adding a moderate number of oscillators with random interactions, once the original ensemble has already undergone the adaptation process, does not produce a substantial change in the collective dynamical state of the system. All these tests point at the robustness of the results presented in Section 3.

Regarding the collective dynamical state achieved by the ensemble after the adaptation process, it is interesting to emphasize that, at the moderate coupling strength considered here, a difference results between the target state of two clusters with opposite phases, on one hand, and ensemble synchronization, on the other. As a result of adaptation, in fact, most oscillators end in pairs of clusters with opposite phases –indicating that an important fraction of repulsive interactions has been redistributed as expected. However, different pairs of clusters have different average frequencies and, therefore, are not mutually synchronized. In other words, there is a certain degree of independence between synchronized clusters and opposite-phase clusters, as depicted in Fig. 6. This "multilevel" clustering may represent a rich regime from the viewpoint of the collective dynamics [12], and deserves further study.

As for the network structure, the results shown in Fig. 7, along with the values obtained for the quantity D, may seem a modest achievement for a Monte Carlo adaptation algorithm on a 50-oscillator ensemble. One should take into account, however, that the algorithm explores the space of possible distributions of $N_1 N_2$ repulsive interactions over the $N(N-1)/2$ oscillator pairs. For $N_1 = 15$ and $N_2 = 35$, identifying the ideal two-group configuration amounts at singling a particular state out of 4.7×10^{361} possibilities! This huge number approximately equals 4^{600}, which indicates that the task is comparable to individualizing a specific 600-nucleotide long genetic message. Note that this figure is not far below the length of some short coding sequences in real genomes [13].

We have shown in this paper that the distinctive scale separation between the mechanisms of mutation and selection which characterize biological evolution –or, equivalently, neural and supervising mechanisms in learning processes– can be emulated by an ensemble of very simple interacting dynamical systems, which adapts to a prescribed form of collective behaviour by gradual changes in its interaction pattern. Admittedly, the two-cluster synchronization state here chosen as the adaptation target is by no means as complex as some of the most elementary functional configurations of biological entities. However, as long as a quantification of the adaptation level –analogous to our two-cluster order parameter z_2– is identified, the same algorithm could be in principle implemented for evolution towards more sophisticated collective dynamics. The same consideration can be applied to systems whose elementary components are dynamically richer that the phase oscillators studied here, such in the case of chaotic units [4], or whose interaction pattern is structurally closer to those observed in real biological networks –typically, much more sparse than our fully connected graphs. Additional dynamical ingredients may include, for instance, the effects of internal fluctuations and noise.

In any case, the quantitative extent and limitations of the correspondence between biological evolution and adaptation in networks of dynamical elements –in particular, with respect to the performance of the adaptation algorithm– as well as the possibility of implementation in other complex systems with different forms of self-organizing collective dynamics, is worth considering in future work.

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